

<!--StartFragment-->RESULT 1
JC8067
mitochondrial C1-tetrahydrofolate synthetase - human
C;Species: Homo sapiens (man)
C;Date: 09-May-2004 #sequence_revision 09-May-2004 #text_change 05-Oct-2004
C;Accession: JC8067
R;Sugiura, T., Nagano, Y., Inoue, T., and Hirotani, K.
Biochem. Biophys. Res. Commun. 315, 204-211, 2004
A;Title: A novel mitochondrial C1-tetrahydrofolate synthetase is upregulated in human colon adenocarcinoma.
A;Reference number: JC8067; PMID: 15013446
A;Accession: JC8067
A;Molecule type: mRNA
A;Residues: 1-978 <SUG>
A;Cross-references: GB:ALL17452
C;Comment: This enzyme, which is a trifunctional enzyme, participates in the progression of colorectal cancer by conferring growth advantage and is a new molecular target for colon cancer therapy. It is important in catalysis of reactions in the one-carbon metabolic pathway and is capable of accelerating cell proliferation.
C;Genetics:
A;Gene: DKFZp586G1517
A;Map position: 6q25.1
C;Superfamily: C1-tetrahydrofolate synthase
C;Keywords: C1-tetrahydrofolate synthetase; colon cancer; one-carbon unit pathway; trifunctional enzyme

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Query Match      100.0%; Score 4998; DB 2; Length 978;
Best Local Similarity 100.0%; Pred. No. 1.3e-289;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Qy 61 CSPGGRTPAARDSIVREVIQNSKEVLLSLQEKNPFKPVLAIIQAGDDNLMQEINQNLAE 120
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Ph 61 CSDGGRTPAARDSIVREVIQNSKEVLLSLQEKNPFKPVLAIIQAGDDNLMQEINQNLAE 120

Qy 181 GVTIDNLGKLVRGDAHECFVSPVAKAVIELLEKSGVNLDGKKILVVGAGHSLEAAQLC 240
|||
Dy 181 GVTIDNLGKLVRGDAHECFVSPVAKAVIELLEKSGVNLDGKKILVVGAGHSLEAAQLC 240

Qy 241 QRKGSMTMSIQWKTQLQSKLHEADIVVLGSPKPEEIPLTWIQPGTTVNCNSHDFLSGV 300
Pb 241 QRKGSMTMSIQWKTQLQSKLHEADIVVLGSPKPEEIPLTWIQPGTTVNCNSHDFLSGV 300

Qy 301 GCGSPRIHFGLIEEDDVLLAALR1QNMVSSGRRWLREQQHRRWLHLCKLQLPLSPVP 360
|||.....|||||.....|||||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Dy 301 GCGSPRIHFGLIEEDDVLLAALR1QNMVSSGRRWLREQQHRRWLHLCKLQLPLSPVP 360

Qy 361 SDIEISRGQTPKAVDVLAKEIIGLLADEIEIYGKS KAKVRLSVLERLKDQADGKYVLVAGI 420
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dy 361 SDIEISRGQTPKAVDVLAKEIIGLLADEIEIYGKS KAKVRLSVLERLKDQADGKYVLVAGI 420

Qy	421	TPTPLGEKSTVTIGLVQALTAAHLNVNSFACLRQPSQGPTFGVKGGAAGGGYAQVIPMEE	480
Db	421	TPTPLGEKSTVTIGLVQALTAAHLNVNSFACLRQPSQGPTFGVKGGAAGGGYAQVIPMEE	480
Qy	481	FNLHLTGDIHAITAANNLAAAIDTRILHENQTDKALYNRLVPLVNGVREFSEIQLARL	540
Db	481	FNLHLTGDIHAITAANNLAAAIDTRILHENQTDKALYNRLVPLVNGVREFSEIQLARL	540
Qy	541	KKLGINKTDPSTLTEEVSFKFARLDIDPSTITWQRVLDTNDRFLRKITIGQGNTEKGHYR	600
Db	541	KKLGINKTDPSTLTEEVSFKFARLDIDPSTITWQRVLDTNDRFLRKITIGQGNTEKGHYR	600
Qy	601	QAQFDIAVASEIMAVLALTDSDLADMKARLGRMVVASDKSGQPVTADDLGVGTALTVLMKD	660
Db	601	QAQFDIAVASEIMAVLALTDSDLADMKARLGRMVVASDKSGQPVTADDLGVGTALTVLMKD	660
Qy	661	AIKPKNLMQTLEGPVVFHAGPFANIAHGNSSVLADKIALKLVGEEGFVVTEAGFGADIGM	720
Db	661	AIKPKNLMQTLEGPVVFHAGPFANIAHGNSSVLADKIALKLVGEEGFVVTEAGFGADIGM	720
Qy	721	EKFFNIKCRASGLVPNVVVLVATVRALKMHGGGPSVTAGVPLKKEYTEENIQLVADGCCN	780
Db	721	EKFFNIKCRASGLVPNVVVLVATVRALKMHGGGPSVTAGVPLKKEYTEENIQLVADGCCN	780
Qy	781	LQKQIQUITQLFGPVVVALNVFKTDRAEIDLVCELAKRAGAFDAVPCYHWSVGGKGCSV	840
Db	781	LQKQIQUITQLFGPVVVALNVFKTDRAEIDLVCELAKRAGAFDAVPCYHWSVGGKGCSV	840
Qy	841	LARAVREAASKRSRFQFLYDVQVPIVDKIRTIAQAVYGAKDIELSPEAQAKIDRYTQQGF	900
Db	841	LARAVREAASKRSRFQFLYDVQVPIVDKIRTIAQAVYGAKDIELSPEAQAKIDRYTQQGF	900
Qy	901	GNLPICMAKTHLSLSHQPDKKGVPRDFILPISDVRASIGAGFIYPLVGMSTMPGLPTRP	960
Db	901	GNLPICMAKTHLSLSHQPDKKGVPRDFILPISDVRASIGAGFIYPLVGMSTMPGLPTRP	960
Qy	961	CFYDIDLDTETEQVKGLF	978
Db	961	CFYDIDLDTETEQVKGLF	978

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